

SEQUENCE LISTING

<110> Allan, Bernard  
Gregoire, Francine  
Lavan, Brian  
Moodie, Shonna  
Metabolex, Inc.

<120> Methods of Diagnosing & Treating Diabetes and Insulin  
Resistance

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<140> US 10/516,635  
<141> 2004-11-03

<150> US 60/386,085  
<151> 2002-06-04

<150> US 60/386,331  
<151> 2002-06-05

<150> WO PCT/US03/17725  
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atttttacac tattgtgaat atttggaaattt gaaacgtgtt atattgttgcataa gaggccccaa 2340

agaattggaa tcctccttaa tttaattgct ttgaagcata gctacaattt gttttgcat 2400  
 tttgttttggaa aggtttaac aaatgactgt atctaggcat ttcattatgc tttgaacttt 2460  
 agtttgcctg cagtttcttg ttagatttggaa aaaattgtat accaatgtgt tttctgtaga 2520  
 ctctaagata cactgcactt tgtagaaaaaaaactgaa gatgaaatat atattgtaaa 2580  
 gaaggatataaagaatctt agataacttc ttgaaaaaaga tggcttatgt catcagtaaa 2640  
 gtacctttat gttatgagga tataatgtgt gctttattga attagaaaaat tagtgaccat 2700  
 tattcacagg tggacaaatg ttgtcctgtt aattatagg agtttttgg ggatgtggag 2760  
 gtagttgggt agaaaaaatta tttagaacatt cactttgtt aacagtattt ctctttatt 2820  
 ctgttatata gtggatgata tacacagtgaa caaaacaaaaa gtacattgtt taataatata 2880  
 agtggaaaat gtcactatataat cttcccatat aacattgtt ttgtatattt ggttagatt 2940  
 totgacatca aaacttggac ccttggaaaaaaaagttt aattaaaaaa aatccttgc 3000  
 acttacaatt tgccacaatataat ttctttgtt gtactttata tcttgttac aataaagaat 3060  
 tccctttggtaaaaaaaa 3085

<210> 8  
 <211> 469  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> human transforming growth factor-beta (TGFB)  
 inducible early growth response (TIEG)

<400> 8  
 Met Glu Glu Arg Met Glu Met Ile Ser Glu Arg Pro Lys Glu Ser Met  
 1 5 10 15

Tyr Ser Trp Asn Lys Thr Ala Glu Lys Ser Asp Phe Glu Ala Val Glu  
 20 25 30

Ala Leu Met Ser Met Ser Cys Ser Trp Lys Ser Asp Phe Lys Lys Tyr  
 35 40 45

Val Glu Asn Arg Pro Val Thr Pro Val Ser Asp Leu Ser Glu Glu Glu  
 50 55 60

Asn Leu Leu Pro Gly Thr Pro Asp Phe His Thr Ile Pro Ala Phe Cys  
 65 70 75 80

Leu Thr Pro Pro Tyr Ser Pro Ser Asp Phe Glu Pro Ser Gln Val Ser  
 85 90 95

Asn Leu Met Ala Pro Ala Pro Ser Thr Val His Phe Lys Ser Leu Ser  
 100 105 110

Asp Thr Ala Lys Pro His Ile Ala Ala Pro Phe Lys Glu Glu Lys  
 115 120 125

Ser Pro Val Ser Ala Pro Lys Leu Pro Lys Ala Gln Ala Thr Ser Val  
 130 135 140

Ile Arg His Thr Ala Asp Ala Gln Leu Cys Asn His Gln Thr Cys Pro  
 145 150 155 160

Met Lys Ala Ala Ser Ile Leu Asn Tyr Gln Asn Asn Ser Phe Arg Arg  
 165 170 175

Arg Thr His Leu Asn Val Glu Ala Ala Arg Lys Asn Ile Pro Cys Ala  
 180 185 190

Ala Val Ser Pro Asn Arg Ser Lys Cys Glu Arg Asn Thr Val Ala Asp  
195 200 205

Val Asp Glu Lys Ala Ser Ala Ala Leu Tyr Asp Phe Ser Val Pro Ser  
210 215 220

Ser Glu Thr Val Ile Cys Arg Ser Gln Pro Ala Pro Val Ser Pro Gln  
225 230 235 240

Gln Lys Ser Val Leu Val Ser Pro Pro Ala Val Ser Ala Gly Gly Val  
245 250 255

Pro Pro Met Pro Val Ile Cys Gln Met Val Pro Leu Pro Ala Asn Asn  
260 265 270

Pro Val Val Thr Thr Val Val Pro Ser Thr Pro Pro Ser Gln Pro Pro  
275 280 285

Ala Val Cys Pro Pro Val Val Phe Met Gly Thr Gln Val Pro Lys Gly  
290 295 300

Ala Val Met Phe Val Val Pro Gln Pro Val Val Gln Ser Ser Lys Pro  
305 310 315 320

Pro Val Val Ser Pro Asn Gly Thr Arg Leu Ser Pro Ile Ala Pro Ala  
325 330 335

Pro Gly Phe Ser Pro Ser Ala Ala Lys Val Thr Pro Gln Ile Asp Ser  
340 345 350

Ser Arg Ile Arg Ser His Ile Cys Ser His Pro Gly Cys Gly Lys Thr  
355 360 365

Tyr Phe Lys Ser Ser His Leu Lys Ala His Thr Arg Thr His Thr Gly  
370 375 380

Glu Lys Pro Phe Ser Cys Ser Trp Lys Gly Cys Glu Arg Arg Phe Ala  
385 390 395 400

Arg Ser Asp Glu Leu Ser Arg His Arg Arg Thr His Thr Gly Glu Lys  
405 410 415

Lys Phe Ala Cys Pro Met Cys Asp Arg Arg Phe Met Arg Ser Asp His  
420 425 430

Leu Thr Lys His Ala Arg Arg His Leu Ser Ala Lys Lys Leu Pro Asn  
435 440 445

Trp Gln Met Glu Val Ser Lys Leu Asn Asp Ile Ala Leu Pro Pro Thr  
450 455 460

Pro Ala Pro Thr Gln  
465

<210> 9  
<211> 3045  
<212> DNA  
<213> Mus musculus



agaagagttt tcttaaaaat tataaaaaat cacgagttac aatttgcaca atatttttg 3000  
ttgaacttta taccttgtt acaataaaga cttttctttg gtata 3045

<210> 10  
<211> 479  
<212> PRT  
<213> Mus musculus

<220>  
<223> mouse transforming growth factor-beta (TGFB)  
inducible early growth response (TIEG) homolog

<400> 10  
Met Leu Asn Phe Gly Ala Ser Leu Gln Gln Ala Ser Glu Gly Lys Met  
1 5 10 15  
  
Glu Leu Ile Ser Glu Lys Pro Arg Glu Gly Met His Pro Trp Asp Lys  
20 25 30  
  
Ala Glu Gln Ser Asp Phe Glu Ala Val Glu Ala Leu Met Ser Met Ser  
35 40 45  
  
Cys Asp Trp Lys Ser His Phe Lys Lys Tyr Leu Glu Asn Arg Pro Val  
50 55 60  
  
Thr Pro Val Ser Asp Thr Ser Glu Asp Asp Ser Leu Leu Pro Gly Thr  
65 70 75 80  
  
Pro Asp Leu Gln Thr Val Pro Ala Phe Cys Leu Thr Pro Pro Tyr Ser  
85 90 95  
  
Pro Ser Asp Phe Glu Pro Ser Gln Gly Ser Asn Leu Thr Ala Ser Ala  
100 105 110  
  
Pro Ser Thr Gly His Phe Lys Ser Phe Ser Asp Ala Ala Lys Pro Pro  
115 120 125  
  
Gly Ala Thr Pro Phe Lys Glu Glu Lys Asn Pro Leu Ala Ala Pro  
130 135 140  
  
Pro Leu Pro Lys Ala Gln Ala Thr Ser Val Ile Arg His Thr Ala Asp  
145 150 155 160  
  
Ala Gln Leu Cys Asn His Gln Ser Cys Pro Val Lys Ala Ala Ser Ile  
165 170 175  
  
Leu Asn Tyr Gln Asp Asn Ser Phe Arg Arg Arg Thr His Gly Asn Val  
180 185 190  
  
Glu Ala Thr Arg Lys Asn Ile Pro Cys Ala Ala Val Ser Pro Asn Arg  
195 200 205  
  
Ser Lys Pro Glu Pro Ser Thr Val Ser Asp Gly Asp Glu Lys Ala Gly  
210 215 220  
  
Ala Ala Leu Tyr Asp Phe Ala Val Pro Ser Ser Glu Thr Val Ile Cys  
225 230 235 240  
  
Arg Ser Gln Pro Ala Pro Ser Ser Pro Val Gln Lys Ser Val Leu Val  
245 250 255

Ser Ser Pro Thr Val Ser Thr Gly Gly Val Pro Pro Leu Pro Val Ile  
 260 265 270  
 Cys Gln Met Val Pro Leu Pro Ala Asn Asn Ser Leu Val Ser Thr Val  
 275 280 285  
 Val Pro Ser Thr Pro Pro Ser Gln Pro Pro Ala Val Cys Ser Pro Val  
 290 295 300  
 Leu Phe Met Gly Thr Gln Val Pro Glu Gly Thr Val Val Phe Val Val  
 305 310 315 320  
 Pro Gln Pro Val Val Gln Ser Pro Arg Pro Pro Val Val Ser Pro Ser  
 325 330 335  
 Gly Thr Arg Leu Ser Pro Ile Ala Pro Ala Pro Gly Phe Ser Pro Ser  
 340 345 350  
 Ala Ala Arg Val Thr Pro Gln Ile Asp Ser Ser Arg Val Arg Ser His  
 355 360 365  
 Ile Cys Ser His Pro Gly Cys Gly Lys Thr Tyr Phe Lys Ser Ser His  
 370 375 380  
 Leu Lys Ala His Val Arg Thr His Thr Gly Glu Lys Pro Phe Ser Cys  
 385 390 395 400  
 Ser Trp Lys Gly Cys Glu Arg Arg Phe Ala Arg Ser Asp Glu Leu Ser  
 405 410 415  
 Arg His Arg Arg Thr His Thr Gly Glu Lys Lys Phe Ala Cys Pro Met  
 420 425 430  
 Cys Asp Arg Arg Phe Met Arg Ser Asp His Leu Thr Lys His Ala Arg  
 435 440 445  
 Arg His Leu Ser Ala Lys Lys Leu Pro Asn Trp Gln Met Glu Val Ser  
 450 455 460  
 Lys Leu Asn Asp Ile Ala Leu Pro Pro Thr Pro Ala Ser Ala Gln  
 465 470 475

<210> 11  
 <211> 3115  
 <212> DNA  
 <213> Rattus norvegicus

<220>  
 <223> rat transforming growth factor-beta (TGFB)  
 inducible early growth response (TIEG) homolog  
 cDNA

<220>  
 <221> CDS  
 <222> (316) .. (1758)  
 <223> TIEG homolog

<400> 11  
 ggagggaaaca cgggcctcg gggtgttac acgctccact gacagagctt cttgcagccg 60  
 ggcagccgt gatcacgcgt ggccccgcca gcccattggc tgaggcctca cacacctttg 120

<210> 12  
<211> 480  
<212> PRT  
<213> *Rattus norvegicus*

<220>  
<223> rat transforming growth factor-beta (TGFB)  
inducible early growth response (TIEG) homolog

<400> 12  
Met Leu Asn Phe Gly Ala Ser Leu Gln Gln Ala Ser Glu Gly Lys Met  
1 5 10 15  
  
Glu Leu Ile Ser Glu Lys Ser Lys Glu Gly Ala His Pro Trp Asp Lys  
20 25 30  
  
Ala Glu Gln Ser Asp Phe Glu Ala Val Glu Ala Leu Met Ser Met Ser  
35 40 45  
  
Cys Asp Trp Lys Ser His Phe Lys Lys Tyr Leu Glu Asn Arg Pro Val  
50 55 60  
  
Thr Pro Val Ser Asp Thr Ser Glu Glu Asp Ser Leu Leu Pro Gly Thr  
65 70 75 80  
  
Pro Asp Leu Gln Thr Val Pro Ala Phe Cys Leu Thr Pro Pro Tyr Ser  
85 90 95  
  
Pro Ser Asp Phe Glu Pro Ser Gln Gly Ser Asn Leu Thr Ala Pro Ala  
100 105 110  
  
Pro Pro Thr Gly His Phe Arg Ser Leu Ser Asp Ala Ala Lys Pro Pro  
115 120 125  
  
Ser Ile Ala Pro Phe Lys Glu Glu Lys Ser Pro Leu Ala Ala Pro  
130 135 140  
  
Pro Leu Pro Lys Ala Gln Ala Thr Ser Val Ile Arg His Thr Ala Asp  
145 150 155 160  
  
Ala Gln Leu Cys Asn His Gln Ser Cys Pro Val Lys Ala Ala Ser Ile  
165 170 175  
  
Leu Asn Tyr Gln Asp Asn Ser Phe Arg Arg Arg Thr His Ile Asn Val  
180 185 190  
  
Glu Ala Thr Arg Lys Asn Ile Pro Cys Ala Ala Val Ser Pro Asn Arg  
195 200 205  
  
Pro Lys Pro Glu Pro Ser Thr Ala Ala Asn Gly Ala Glu Lys Ala Gly  
210 215 220  
  
Thr Ala Pro Tyr Asp Phe Ala Val Pro Ser Ser Glu Thr Val Ile Cys  
225 230 235 240  
  
Arg Ser Ser Gln Pro Ala Pro Thr Ser Pro Val Gln Lys Ser Val Leu  
245 250 255  
  
Met Ser Ser Pro Thr Val Ser Thr Gly Gly Val Pro Pro Leu Pro Val  
260 265 270  
  
Ile Cys Gln Met Val Pro Leu Pro Ala Asn Asn Ser Leu Val Thr Thr  
275 280 285  
  
Val Val Pro Ser Ser Pro Pro Ser Gln Pro Pro Ala Val Cys Ser Pro  
290 295 300  
  
Val Leu Phe Met Gly Thr Gln Val Pro Lys Gly Thr Val Met Phe Val  
305 310 315 320

Val	Pro	Gln	Pro	Val	Val	Gln	Ser	Pro	Lys	Pro	Pro	Val	Val	Ser	Pro
325									330					335	
Asn	Gly	Thr	Arg	Leu	Ser	Pro	Ile	Ala	Pro	Ala	Pro	Gly	Phe	Ser	Pro
340									345					350	
Ser	Ala	Ala	Arg	Val	Thr	Pro	Gln	Ile	Asp	Ser	Ser	Arg	Val	Arg	Ser
355									360					365	
His	Ile	Cys	Ser	His	Pro	Gly	Cys	Gly	Lys	Thr	Tyr	Phe	Lys	Ser	Ser
370									375					380	
His	Leu	Lys	Ala	His	Val	Arg	Thr	His	Thr	Gly	Glu	Lys	Pro	Phe	Ser
385									390					395	
Cys	Ser	Trp	Lys	Gly	Cys	Glu	Arg	Arg	Phe	Ala	Arg	Ser	Asp	Glu	Leu
405									410					415	
Ser	Arg	His	Arg	Arg	Thr	His	Thr	Gly	Glu	Lys	Lys	Phe	Ala	Cys	Pro
420									425					430	
Met	Cys	Asp	Arg	Arg	Phe	Met	Arg	Ser	Asp	His	Leu	Thr	Lys	His	Ala
435									440					445	
Arg	Arg	His	Leu	Ser	Ala	Lys	Lys	Leu	Pro	Asn	Trp	Gln	Met	Glu	Val
450									455					460	
Ser	Lys	Leu	Asn	Asp	Ile	Ala	Leu	Pro	Pro	Ala	Thr	Ala	Ser	Ala	Gln
465									470					475	
															480

<210> 13  
 <211> 2872  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> human transforming growth factor-beta (TGFB)  
 inducible early growth response (TIEG) splice  
 variant cDNA

<220>  
 <221> CDS  
 <222> (87)..(1529)  
 <223> TIEG splice variant

<400> 13  
 gaattcggca cgagcgcccc tctgtggcca agcagccagc agcctagcag ccagtcagct 60  
 tgccgcggc ggccaaagcag ccaaccatgc tcaacttcgg tgcctctctc cagcagactg 120  
 cggaggaaag aatggaaatg atttctgaaa ggccaaaaga gagttatgtat tcctggaaaca 180  
 aaactgcaga gaaaagtgtat tttgaagctg tagaagact tatgtcaatg agctgcagg 240  
 ggaagtctga ttttaagaaa tacgttggaaa acagacctgt tacaccagta tctgattttgt 300  
 cagaggaaga gaatctgctt ccggaaacac ctgattttca tacaatccca gcattttgtt 360  
 tgactccacc ttacagtccct tctgactttg aaccctctca agtgtcaaat ctgatggcac 420  
 cagcgccatc tactgtacac ttcaagtccac tctcagatac tgccaaacct cacattgccc 480  
 cacctttcaa agaggaagaa aagagccccag tatctgcccc caaactcccc aaagctcagg 540  
 caacaagtgt gattcgtcat acagctgatg cccagctatg taaccaccag acctgccccaa 600  
 taaaaggcagc cagcatcctc aactatcaga acaattcttt tagaagaaga acccacctaa 660  
 atgttgaggc tgcaagaaag aacataccat gtggcgctgt gtcacccaaac agatccaaat 720  
 gtgagagaaa cacagtggca gatgttgatg agaaagcaag tgctgcactt tatgacttt 780  
 ctgtgccttc ctcagagacg gtcatctgca ggtctcagcc agccctgtg tccccacaac 840

agaagtca... gttggctctt ccacctgc... tatctgcagg gggagtgcc... cctatgc... 900  
tcatctgcca gatggttccc cttcc... acaaccctgt t... g... gtcgttccc... 960  
gcactcctcc cagccagcca ccagg... gcccccc... t... g... ggcacaca... 1020  
tccccaaagg cgctgtcat... tttgtggta... cccagcc... t... g... tcaa... 1080  
cggtggtag cccgaatggc accagact... cttcc... attcatca... gataagg... cacatctg... 1140  
cttcagcagc aaaagtcact cctcagatt... aaagttcc... tctgaagg... cacacgag... 1200  
gccaccagg atgtggcaag acatactt... aaagttcc... tctgaagg... cacacgag... 1260  
cgcacacagg agaaaagcct ttcagctg... gctggaaagg ttgtgaaagg aggttgc... 1320  
gttctgatga actgtccaga cacagg... cccacac... tgagaagaaa tttgcgtg... 1380  
ccatgtgtga cccgcgg... atgaggag... accatttg... caagcatg... cggcgc... 1440  
tatcagccaa gaagctacca aactggc... t... g... gacattg... 1500  
tacctccaac cctgtctccc acacagt... agaccgg... gtgaagag... agaacta... 1560  
ttggtctcag cgggagccag tgg... aaaaatg... cactg... ctgtg... 1620  
acaacgtggg cttaaagcag aagccc... gcctgg... aaggccc... ctgggtt... 1680  
tgactaaaag ggcttcggcc acaggcag... cacagaaagg cagg... ttcttatc... 1740  
ataagagaga tgagaaagct ttattc... t... g... t... cagatg... 1800  
caacacaggt agcacagatt ttgaatctg... gtgcata... gttactt... ttttgc... 1860  
tatacttgag accaactttt caatgtgatt... cttctaa... actgg... agaatatg... 1920  
agctggaaagg aaataaaacat tacgtacag acatgg... gtaaaatg... tttgtatt... 1980  
tacaaatatt gtcatcttt tctagagtt... t... t... cttcc... 2040  
aacatcg... atgttagt... taaatata... tagaactatc... attttac... tattgt... 2100  
at... gaa... gaa... atattg... ggggccc... agaattgg... tcctc... 2160  
ttaattg... ttgaagc... gctacaattt... gttttg... tttgtt... aaagtt... 2220  
aaatgactgt atctagg... ttcattatg... ttgaactt... agtttgc... cagttc... 2280  
ttagattt... aaaattgt... accaatgt... tttctgt... ctctaa... cactg... 2340  
tgttagaaa aaaaactg... gatgaaat... atattgt... gatgaaat... taagaat... 2400  
agataactt... ttgaaa... tggctt... catcagta... gtac... 2460  
tataatgt... gctt... attagaa... tagt... tattc... tggaca... 2520  
ttcgtcctg... taatttata... gagttt... gggatgt... ggtag... tagaaa... 2580  
attagaacat tca... t... t... tctctt... tctgtt... agtgg... 2640  
atcacac... gcaaa... agtacatt... t... t... taaa... tagt... 2700  
tctcc... taacatt... tttgtat... ggggtg... ttctg... aaaactt... 2760  
cccttgg... acaaa... agt... taatt... aaatc... gactt... ttgcaca... 2820  
tttctt... t... t... t... t... caataa... ttc... ca... 2872

<210> 14  
<211> 480  
<212> PRT  
<213> *Homo sapiens*

<220>  
<223> human transforming growth factor-beta (TGF $\beta$ )  
inducible early growth response (TIEG) splice  
variant

<400> 14  
Met Leu Asn Phe Gly Ala Ser Leu Gln Gln Thr Ala Glu Glu Arg Met  
1 5 10 15

Glu Met Ile Ser Glu Arg Pro Lys Glu Ser Met Tyr Ser Trp Asn Lys  
20 25 30

Thr Ala Glu Lys Ser Asp Phe Glu Ala Val Glu Ala Leu Met Ser Met  
35 40 45

Ser Cys Ser Trp Lys Ser Asp Phe Lys Lys Tyr Val Glu Asn Arg Pro  
50 55 60

Thr Pro Asp Phe His Thr Ile Pro Ala Phe Cys Leu Thr Pro Pro Tyr  
85 90 95

Ser Pro Ser Asp Phe Glu Pro Ser Gln Val Ser Asn Leu Met Ala Pro  
100 105 110

Ala Pro Ser Thr Val His Phe Lys Ser Leu Ser Asp Thr Ala Lys Pro  
115 120 125

His Ile Ala Ala Pro Phe Lys Glu Glu Lys Ser Pro Val Ser Ala  
130 135 140

Pro Lys Leu Pro Lys Ala Gln Ala Thr Ser Val Ile Arg His Thr Ala  
145 150 155 160

Asp Ala Gln Leu Cys Asn His Gln Thr Cys Pro Met Lys Ala Ala Ser  
165 170 175

Ile Leu Asn Tyr Gln Asn Asn Ser Phe Arg Arg Arg Thr His Leu Asn  
180 185 190

Val Glu Ala Ala Arg Lys Asn Ile Pro Cys Ala Ala Val Ser Pro Asn  
195 200 205

Arg Ser Lys Cys Glu Arg Asn Thr Val Ala Asp Val Asp Glu Lys Ala  
210 215 220

Ser Ala Ala Leu Tyr Asp Phe Ser Val Pro Ser Ser Glu Thr Val Ile  
225 230 235 240

Cys Arg Ser Gln Pro Ala Pro Val Ser Pro Gln Gln Lys Ser Val Leu  
245 250 255

Val Ser Pro Pro Ala Val Ser Ala Gly Gly Val Pro Pro Met Pro Val  
260 265 270

Ile Cys Gln Met Val Pro Leu Pro Ala Asn Asn Pro Val Val Thr Thr  
275 280 285

Val Val Pro Ser Thr Pro Pro Ser Gln Pro Pro Ala Val Cys Pro Pro  
290 295 300

Val Val Phe Met Gly Thr Gln Val Pro Lys Gly Ala Val Met Phe Val  
305 310 315 320

Val Pro Gln Pro Val Val Gln Ser Ser Lys Pro Pro Val Val Ser Pro  
325 330 335

Asn Gly Thr Arg Leu Ser Pro Ile Ala Pro Ala Pro Gly Phe Ser Pro  
340 345 350

Ser Ala Ala Lys Val Thr Pro Gln Ile Asp Ser Ser Arg Ile Arg Ser  
355 360 365

His Ile Cys Ser His Pro Gly Cys Gly Lys Thr Tyr Phe Lys Ser Ser  
370 375 380

His Leu Lys Ala His Thr Arg Thr His Thr Gly Glu Lys Pro Phe Ser  
385 390 395 400

Cys Ser Trp Lys Gly Cys Glu Arg Arg Phe Ala Arg Ser Asp Glu Leu  
405 410 415

Ser Arg His Arg Arg Thr His Thr Gly Glu Lys Lys Phe Ala Cys Pro  
420 425 430

Met Cys Asp Arg Arg Phe Met Arg Ser Asp His Leu Thr Lys His Ala  
435 440 445

Arg Arg His Leu Ser Ala Lys Lys Leu Pro Asn Trp Gln Met Glu Val  
450 455 460

Ser Lys Leu Asn Asp Ile Ala Leu Pro Pro Thr Pro Ala Pro Thr Gln  
465 470 475 480

<210> 15

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:hexahistidine  
(His) affinity tag

<400> 15

His His His His His  
1 5

<210> 16

<211> 200

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:poly-Gly  
flexible linker

<220>

<221> MOD\_RES

<222> (6)..(200)

<223> Gly residues from position 6 to 200 may be present  
or absent

<400> 16

Gly  
1 5 10 15

Gly  
20 25 30

Gly  
35 40 45

Gly  
50 55 60

Gly  
65 70 75 80

Gly  
85 90 95

Gly  
100 105 110

Gly  
115 120 125

Gly  
130 135 140

Gly  
145 150 155 160

Gly  
165 170 175

Gly  
180 185 190

Gly Gly Gly Gly Gly Gly Gly  
195 200